

SEQUENCE LISTING

<110> Sheppard, Paul O.
Gilbertson, Debra G.

<120> SECRETED PROTEINS ENCODED BY HUMAN CHROMOSOME 13

<130> 97-38C1

<150> 60/053,613

<151> 1997-07-24

<150> 09/122,383

<151> 1998-07-24

<160> 19

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1486

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (47)...(1084)

<400> 1

gaattcggca cgagggcagg aggtagacac ggcacagggc gccgag atg cgg cgg 55
Met Arg Arg

1

ggc gcg ggc gcg gct cgg gga cgc gct tcc tgg tgc tgg gcg ctg gcg 103
Gly Ala Gly Ala Ala Arg Gly Arg Ala Ser Trp Cys Trp Ala Leu Ala
5 10 15

ctg ctt tgg ctc gcg gtg gtt ccg ggc tgg tcc cgg gtc tcg ggc atc 151
Leu Leu Trp Leu Ala Val Val Pro Gly Trp Ser Arg Val Ser Gly Ile
20 25 30 35

ccc tcc cgg cgc cac tgg ccg gtg ccc tac aag cgc ttt gac ttc cgt 199

40030050 110503

Pro	Ser	Arg	Arg	His	Trp	Pro	Val	Pro	Tyr	Lys	Arg	Phe	Asp	Phe	Arg	
				40					45					50		
cca	aaa	cct	gat	cct	tat	tgt	caa	gct	aag	tat	act	ttc	tgt	cca	act	247
Pro	Lys	Pro	Asp	Pro	Tyr	Cys	Gln	Ala	Lys	Tyr	Thr	Phe	Cys	Pro	Thr	
			55				60					65				
ggc	tca	cct	atc	cca	gtt	atg	gag	ggt	gat	gat	gac	att	gaa	gtt	ttt	295
Gly	Ser	Pro	Ile	Pro	Val	Met	Glu	Gly	Asp	Asp	Asp	Ile	Glu	Val	Phe	
		70				75					80					
cga	tta	caa	gcc	cca	gta	tgg	gaa	ttt	aaa	tat	gga	gac	ctc	ctg	gga	343
Arg	Leu	Gln	Ala	Pro	Val	Trp	Glu	Phe	Lys	Tyr	Gly	Asp	Leu	Leu	Gly	
		85				90					95					
cac	ttg	aaa	att	atg	cat	gat	gcc	att	gga	ttc	aga	agt	aca	tta	act	391
His	Leu	Lys	Ile	Met	His	Asp	Ala	Ile	Gly	Phe	Arg	Ser	Thr	Leu	Thr	
100					105				110					115		
ggc	aag	aac	tac	aca	atg	gaa	tgg	tat	gaa	ctt	ttc	caa	ctt	ggc	aac	439
Gly	Lys	Asn	Tyr	Thr	Met	Glu	Trp	Tyr	Glu	Leu	Phe	Gln	Leu	Gly	Asn	
			120					125				130				
tgt	aca	ttt	ccc	cat	ctc	cga	cct	gaa	atg	gat	gcc	cct	ttc	tgg	tgt	487
Cys	Thr	Phe	Pro	His	Leu	Arg	Pro	Glu	Met	Asp	Ala	Pro	Phe	Trp	Cys	
			135				140					145				
aat	caa	ggc	gct	gcc	tgc	ttt	ttt	gag	gga	att	gat	gat	gtt	cac	tgg	535
Asn	Gln	Gly	Ala	Ala	Cys	Phe	Phe	Glu	Gly	Ile	Asp	Asp	Val	His	Trp	
		150				155				160						
aag	gaa	aat	ggg	aca	tta	gtt	caa	gta	gca	act	ata	tca	gga	aac	atg	583
Lys	Glu	Asn	Gly	Thr	Leu	Val	Gln	Val	Ala	Thr	Ile	Ser	Gly	Asn	Met	
	165				170					175						
ttc	aac	caa	atg	gca	aag	tgg	gtg	aaa	cag	gac	aat	gaa	aca	gga	att	631
Phe	Asn	Gln	Met	Ala	Lys	Trp	Val	Lys	Gln	Asp	Asn	Glu	Thr	Gly	Ile	
180					185				190					195		
tat	tat	gag	aca	tgg	aat	gta	aaa	gcc	agc	cca	gaa	aag	ggg	gca	gag	679
Tyr	Tyr	Glu	Thr	Trp	Asn	Val	Lys	Ala	Ser	Pro	Glu	Lys	Gly	Ala	Glu	
			200					205					210			

aca tgg ttt gat tcc tac gac tgt tcc aaa ttt gtg tta agg acc ttt 727
 Thr Trp Phe Asp Ser Tyr Asp Cys Ser Lys Phe Val Leu Arg Thr Phe
 215 220 225

aac aag ttg gct gaa ttt gga gca gag ttc aag aac ata gaa acc aac 775
 Asn Lys Leu Ala Glu Phe Gly Ala Glu Phe Lys Asn Ile Glu Thr Asn
 230 235 240

tat aca aga ata ttt ctt tac agt gga gaa cct act tat ctg gga aat 823
 Tyr Thr Arg Ile Phe Leu Tyr Ser Gly Glu Pro Thr Tyr Leu Gly Asn
 245 250 255

gaa aca tct gtt ttt ggg cca aca gga aac aag act ctt ggt tta gcc 871
 Glu Thr Ser Val Phe Gly Pro Thr Gly Asn Lys Thr Leu Gly Leu Ala
 260 265 270 275

ata aaa aga ttt tat tac ccc ttc aaa cca cat ttg cca act aaa gaa 919
 Ile Lys Arg Phe Tyr Tyr Pro Phe Lys Pro His Leu Pro Thr Lys Glu
 280 285 290

ttt ctg ttg agt ctc ttg caa att ttt gat gca gtg att gtg cac aaa 967
 Phe Leu Leu Ser Leu Leu Gln Ile Phe Asp Ala Val Ile Val His Lys
 295 300 305

cag ttc tat ttg ttt tat aat ttt gaa tat tgg ttt tta cct atg aaa 1015
 Gln Phe Tyr Leu Phe Tyr Asn Phe Glu Tyr Trp Phe Leu Pro Met Lys
 310 315 320

ttc cct ttt att aaa ata aca tat gaa gaa atc cct tta cct atc aga 1063
 Phe Pro Phe Ile Lys Ile Thr Tyr Glu Glu Ile Pro Leu Pro Ile Arg
 325 330 335

aac aaa aca ctc tct ggt tta taaaacacct taattctact gctctttttt 1114
 Asn Lys Thr Leu Ser Gly Leu
 340 345

tctccaatca ccagcatctg tttttcaggg ggtgatttta cttttgtgaa ttccttagcc 1174
 tttcttcctt ggtgcataaa gttaaaatgc acatcagcag aattgctgca tattaacatc 1234
 tcaggactct tctcttgtaa agaagctgaa attcgtacta tattggccaa agtgagcgag 1294
 ttaggtgatc ttggtttcaa tttccgagcc tttgttaata tggagaatta tggttcatat 1354
 cagttatgta ggacctttgg acccagggtc ctacagatag atatggtgtg cccagatttt 1414
 aaaaatacct tcaaaaataa aaaatacatt cagtgacaaa aaaaaaaaaa aaaaaatagc 1474
 ggccgcctcg ag 1486

<210> 2
 <211> 346
 <212> PRT
 <213> Homo sapien

<400> 2

Met	Arg	Arg	Gly	Ala	Gly	Ala	Ala	Arg	Gly	Arg	Ala	Ser	Trp	Cys	Trp
1				5					10					15	
Ala	Leu	Ala	Leu	Leu	Trp	Leu	Ala	Val	Val	Pro	Gly	Trp	Ser	Arg	Val
			20					25					30		
Ser	Gly	Ile	Pro	Ser	Arg	Arg	His	Trp	Pro	Val	Pro	Tyr	Lys	Arg	Phe
		35					40					45			
Asp	Phe	Arg	Pro	Lys	Pro	Asp	Pro	Tyr	Cys	Gln	Ala	Lys	Tyr	Thr	Phe
	50					55				60					
Cys	Pro	Thr	Gly	Ser	Pro	Ile	Pro	Val	Met	Glu	Gly	Asp	Asp	Asp	Ile
65					70					75					80
Glu	Val	Phe	Arg	Leu	Gln	Ala	Pro	Val	Trp	Glu	Phe	Lys	Tyr	Gly	Asp
				85					90					95	
Leu	Leu	Gly	His	Leu	Lys	Ile	Met	His	Asp	Ala	Ile	Gly	Phe	Arg	Ser
			100					105					110		
Thr	Leu	Thr	Gly	Lys	Asn	Tyr	Thr	Met	Glu	Trp	Tyr	Glu	Leu	Phe	Gln
		115					120					125			
Leu	Gly	Asn	Cys	Thr	Phe	Pro	His	Leu	Arg	Pro	Glu	Met	Asp	Ala	Pro
	130					135					140				
Phe	Trp	Cys	Asn	Gln	Gly	Ala	Ala	Cys	Phe	Phe	Glu	Gly	Ile	Asp	Asp
145				150					155					160	
Val	His	Trp	Lys	Glu	Asn	Gly	Thr	Leu	Val	Gln	Val	Ala	Thr	Ile	Ser
			165					170						175	
Gly	Asn	Met	Phe	Asn	Gln	Met	Ala	Lys	Trp	Val	Lys	Gln	Asp	Asn	Glu
	180					185						190			
Thr	Gly	Ile	Tyr	Tyr	Glu	Thr	Trp	Asn	Val	Lys	Ala	Ser	Pro	Glu	Lys
	195					200						205			
Gly	Ala	Glu	Thr	Trp	Phe	Asp	Ser	Tyr	Asp	Cys	Ser	Lys	Phe	Val	Leu
	210				215				220						
Arg	Thr	Phe	Asn	Lys	Leu	Ala	Glu	Phe	Gly	Ala	Glu	Phe	Lys	Asn	Ile
225				230				235						240	
Glu	Thr	Asn	Tyr	Thr	Arg	Ile	Phe	Leu	Tyr	Ser	Gly	Glu	Pro	Thr	Tyr
			245					250						255	
Leu	Gly	Asn	Glu	Thr	Ser	Val	Phe	Gly	Pro	Thr	Gly	Asn	Lys	Thr	Leu
		260					265					270			
Gly	Leu	Ala	Ile	Lys	Arg	Phe	Tyr	Tyr	Pro	Phe	Lys	Pro	His	Leu	Pro
	275						280					285			

Thr Lys Glu Phe Leu Leu Ser Leu Leu Gln Ile Phe Asp Ala Val Ile
 290 295 300
 Val His Lys Gln Phe Tyr Leu Phe Tyr Asn Phe Glu Tyr Trp Phe Leu
 305 310 315 320
 Pro Met Lys Phe Pro Phe Ile Lys Ile Thr Tyr Glu Glu Ile Pro Leu
 325 330 335
 Pro Ile Arg Asn Lys Thr Leu Ser Gly Leu
 340 345

<210> 3
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC976

<400> 3
 cgttgtaaaa cgacggcc 18

<210> 4
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC447

<400> 4
 taacaatttc acacagg 17

<210> 5
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC14487

<400> 5
 gattccgtc caaacctga 20

<210> 6

<211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC14716

<400> 6
 aggggcatcc atttcaggtg 20

<210> 7
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC14712

<400> 7
 atggctaaac caagagtctt 20

<210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC14710

<400> 8
 gggtgaaaca ggacaatgaa 20

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC14488

<400> 9
 ttatgcacca aggaagaaag 20

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC14711

<400> 10
 ttttctccaa tcaccagcat 20

<210> 11
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC14430

<400> 11
 gtacatttcc ccatctcc 18

<210> 12
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC14431

<400> 12
 ccattttcct tccagtga 18

<210> 13
 <211> 1038
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide sequence encoding zsig46
 polypeptide of SEQ ID NO:2

<400> 13

atgmgnmgng gngcnggngc ngcnmgnggn mgngcnwsnt ggtgytgggc nytngcnytn 60
 ytntggytng cngtngtncc nggntggwsn mgngtnwsng gnathccnws nmgnmgncay 120
 tggccngtnc cntayaarmg nttygaytty mgncnaarc cngayccnta ytgycargcn 180
 aartayacnt tytgyccnac nggnwsnccn athccngtna tggarggnga ygaygayath 240
 gargtnttym gnytnargc nccngtntgg garttyaart ayggngayyt nytnggncay 300
 ytnaaratha tgcaygaygc nathggntty mgnwsnacny tnacnggnaa raaytayacn 360
 atggartggt aygaryntt ycarytnggn aaytgyacnt tyccncayyt nmgnccngar 420
 atggaygcnc cnttytggtg yaaycarggn gcngcntgyt tyttygargg nathgaygay 480
 gtncaytgga argaraaygg nacnytngtn cargtngcna cnathwsngg naayatgtty 540
 aaycaratgg cnaartgggt naarcargay aaygaracng gnathtayta ygaracntgg 600
 aaygtnaarg cnwsnccnga raarggngcn garacntggt tygaywsnta ygaytgywsn 660
 aarttygtty tnmgnacntt yaayaarytn gcngarttyg gngcngartt yaaraayath 720
 garacnaayt ayacnmgnat httytntay wsgngngarc cnacntayyt nggnaaygar 780
 acnwsngtnt tyggncnac nggnaayaar acnytnggny tngcnathaa rmgnttytay 840
 tayccnttya arccncayyt nccnacnaar garttyytny tnwsnytnyt ncarathtty 900
 gaygcngtna thgtncayaa rcarttytay ytnttytaya aytytgarta ytggttyytn 960
 ccnatgaart tyccnttyat haarathacn taygargara thccnytncc nathmgnaay 1020
 aaracnytnw snggnytn 1038

<210> 14

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Glu-Glu affinity tag peptide

<400> 14

Glu Glu Tyr Met Pro Met Glu

1

5

<210> 15

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC14695

<400> 15

taactcgagg agatgcggcg gggcg

25

<210> 16

